

SEQUENCE LISTING

<110> Hinuma, Shuji
MARUYAMA, Minoru
FUJII, Ryo

<120> Novel Use of EDG Receptor

<130> 3127USOP

<150> PCT/JP2003/015836

<151> 2003-12-11

<150> JP 2002-361415

<151> 2002-12-12

<160> 45

<210> 1

<211> 364

<212> PRT

<213> human

<400> 1

Met	Ala	Ala	Ile	Ser	Thr	Ser	Ile	Pro	Val	Ile	Ser	Gln	Pro	Gln	Phe
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Thr	Ala	Met	Asn	Glu	Pro	Gln	Cys	Phe	Tyr	Asn	Glu	Ser	Ile	Ala	Phe
			20					25					30		
Phe	Tyr	Asn	Arg	Ser	Gly	Lys	His	Leu	Ala	Thr	Glu	Trp	Asn	Thr	Val
			35					40					45		
Ser	Lys	Leu	Val	Met	Gly	Leu	Gly	Ile	Thr	Val	Cys	Ile	Phe	Ile	Met
			50					55					60		
Leu	Ala	Asn	Leu	Leu	Val	Met	Val	Ala	Ile	Tyr	Val	Asn	Arg	Arg	Phe
			65					70					75		80
His	Phe	Pro	Ile	Tyr	Tyr	Leu	Met	Ala	Asn	Leu	Ala	Ala	Ala	Asp	Phe
								85					90		95
Phe	Ala	Gly	Leu	Ala	Tyr	Phe	Tyr	Leu	Met	Phe	Asn	Thr	Gly	Pro	Asn

100	105	110
Thr Arg Arg Leu Thr Val Ser Thr Trp Leu Leu Arg Gln Gly Leu Ile		
115	120	125
Asp Thr Ser Leu Thr Ala Ser Val Ala Asn Leu Leu Ala Ile Ala Ile		
130	135	140
Glu Arg His Ile Thr Val Phe Arg Met Gln Leu His Thr Arg Met Ser		
145	150	155
Asn Arg Arg Val Val Val Val Ile Val Val Ile Trp Thr Met Ala Ile		
165	170	175
Val Met Gly Ala Ile Pro Ser Val Gly Trp Asn Cys Ile Cys Asp Ile		
180	185	190
Glu Asn Cys Ser Asn Met Ala Pro Leu Tyr Ser Asp Ser Tyr Leu Val		
195	200	205
Phe Trp Ala Ile Phe Asn Leu Val Thr Phe Val Val Met Val Val Leu		
210	215	220
Tyr Ala His Ile Phe Gly Tyr Val Arg Gln Arg Thr Met Arg Met Ser		
225	230	235
Arg His Ser Ser Gly Pro Arg Arg Asn Arg Asp Thr Met Met Ser Leu		
245	250	255
Leu Lys Thr Val Val Ile Val Leu Gly Ala Phe Ile Ile Cys Trp Thr		
260	265	270
Pro Gly Leu Val Leu Leu Leu Leu Asp Val Cys Cys Pro Gln Cys Asp		
275	280	285
Val Leu Ala Tyr Glu Lys Phe Phe Leu Leu Leu Ala Glu Phe Asn Ser		
290	295	300
Ala Met Asn Pro Ile Ile Tyr Ser Tyr Arg Asp Lys Glu Met Ser Ala		
305	310	315
Thr Phe Arg Gln Ile Leu Cys Cys Gln Arg Ser Glu Asn Pro Thr Gly		
325	330	335
Pro Thr Glu Gly Ser Asp Arg Ser Ala Ser Ser Leu Asn His Thr Ile		
340	345	350
Leu Ala Gly Val His Ser Asn Asp His Ser Val Val		
355	360	

<210> 2

<211> 1092

<212> DNA

<213> human

<400> 2

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cttgccacag aatggaacac agtcagcaag ctggtgatgg gacttggaat cactgtttgt   180
atcttcatca tgttgccaa cctattggtc atggtggcaa tctatgtcaa ccgccgttc   240
cattttccta tttattacct aatggctaata ctggctgctg cagacttctt tgctgggttg   300
gcctacttct atctcatgtt caacacagga cccaatactc ggagactgac tgtagcaca   360
tggtccctgc gtcagggcct cattgacacc agcctgacgg catctgtggc caacttactg   420
gctattgcaa tcgagaggca cattacggtt ttccgcatgc agctccacac acggatgagc   480
aaccggcggg tagtggtggt cattgtggtc atctggacta tggccatcgt tatgggtgct   540
ataccagtg tgggtggaa ctgtatctgt gatattgaaa attgttcaa catggcaccc   600
ctctacagtg actcttactt agtcttctgg gccattttca acttggtgac ctttgtggta   660
atggtgggtc tctatgtca catctttggc tatgttcgcc agaggactat gagaatgtct   720
cggcatagtt ctggaccccg gcggaatcgg gataccatga tgagtcttct gaagactgtg   780
gtcattgtgc ttggggcctt tatcatctgc tggactcctg gatiggtttt gttacttcta   840
gacgtgtgct gtccacagtg cgacgtgctg gcctatgaga aattcttctt tctccttgct   900
gaattcaact ctgcatgaa ccccatcatt tactcctacc gcgacaaaga aatgagcgcc   960
acctttaggc agatcctctg ctgccagcgc agtgagaacc ccaccggccc cacagaaggc  1020
tcagaccgct cggcttctc cctcaaccac accatcttgg ctggagtcca cagcaatgac  1080
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<210> 3

<211> 364

<212> PRT

<213> Rat

<400> 3

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Thr Ala Met Asn Glu Gln Gln Cys Phe Tyr Asn Glu Ser Ile Ala Phe
      20              25              30
Phe Tyr Asn Arg Ser Gly Lys Tyr Leu Ala Thr Glu Trp Asn Thr Val
      35              40              45
Ser Lys Leu Val Met Gly Leu Gly Ile Thr Val Cys Val Phe Ile Met
      50              55              60

```

Leu Ala Asn Leu Leu Val Met Val Ala Ile Tyr Val Asn Arg Arg Phe
 65 70 75 80
 His Phe Pro Ile Tyr Tyr Leu Met Ala Asn Leu Ala Ala Asp Phe
 85 90 95
 Phe Ala Gly Leu Ala Tyr Phe Tyr Leu Met Phe Asn Thr Gly Pro Asn
 100 105 110
 Thr Arg Arg Leu Thr Val Ser Thr Trp Leu Leu Arg Gln Gly Leu Ile
 115 120 125
 Asp Thr Ser Leu Thr Ala Ser Val Ala Asn Leu Leu Ala Ile Ala Ile
 130 135 140
 Glu Arg His Ile Thr Val Phe Arg Met Gln Leu His Thr Arg Met Ser
 145 150 155 160
 Asn Arg Arg Val Val Val Val Ile Val Val Ile Trp Thr Met Ala Ile
 165 170 175
 Val Met Gly Ala Ile Pro Ser Val Gly Trp Asn Cys Ile Cys Asp Ile
 180 185 190
 Asp His Cys Ser Asn Met Ala Pro Leu Tyr Ser Asp Ser Tyr Leu Val
 195 200 205
 Phe Trp Ala Ile Phe Asn Leu Val Thr Phe Val Val Met Val Val Leu
 210 215 220
 Tyr Ala His Ile Phe Gly Tyr Val Arg Gln Arg Thr Met Arg Met Ser
 225 230 235 240
 Arg His Ser Ser Gly Pro Arg Arg Asn Arg Asp Thr Met Met Ser Leu
 245 250 255
 Leu Lys Thr Val Val Ile Val Leu Gly Ala Phe Ile Val Cys Trp Thr
 260 265 270
 Pro Gly Leu Val Leu Leu Leu Leu Asp Val Cys Cys Pro Gln Cys Asp
 275 280 285
 Val Leu Ala Tyr Glu Lys Phe Phe Leu Leu Leu Ala Glu Phe Asn Ser
 290 295 300
 Ala Met Asn Pro Ile Ile Tyr Ser Tyr Arg Asp Lys Glu Met Ser Ala
 305 310 315 320
 Thr Phe Arg Gln Ile Leu Cys Cys Gln Arg Asn Glu Asn Pro Asn Gly
 325 330 335
 Pro Thr Glu Gly Ser Asp Arg Ser Ala Ser Ser Leu Asn His Thr Ile
 340 345 350
 Leu Ala Gly Val His Ser Asn Asp His Ser Val Val

355

360

<210> 4

<211> 1092

<212> DNA

<213> Rat

<400> 4

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ctagccacag aatggaacac tgtgagcaag ctggtgatgg gactgggcat cactgtctgc   180
gtgttcatca tcttgcccaa tctactggtc atggtggcaa ttacgtcaa ccgccgttc   240
catttcccta ttattactt gatggccaac ctggtgtctg cagacttctt cgctggactg   300
gcctacttct accgatgtt caacacggga cctaataccc ggagactgac cgtgagcaca   360
tggtctctcc ggcagggcct catcgacacc agcctgacgg cttctgtggc caacctgtg   420
gccattgcca tcgagaggca catcacagt ttccgaatgc agctccatac acgaatgagc   480
aaccgacgtg tgggtggtgt gattgtagtc atctggacta tggccattgt gatgggtgcc   540
ataccagctg tgggtggaa ctgcatctgt gatatcgatc attgttccaa catggcgccc   600
ctctacagtg actcctactt agtcttctgg gccattttca acctgggtgac ctttgtggtc   660
atggtgggtc tctacgtca catctttggc tatgttcgcc agaggactat gagaatgtcc   720
cggcatagtt ctggaccag gaggaatcgg gacaccatga tgagccttct gaagactgtg   780
gtcattgtgc tgggtgctt tattgtctgc tggactccgg gatttgtctt gctactgtc   840
gatgtgtgtt gcccgagctg cgatgtcctg gcctatgaga agttcttctt cctcctggcc   900
gagttcaact ctgctatgaa cccatcatc tactcctacc gcgacaaaga gatgagcgcc   960
accttcaggc agatcctgtg ttgccagcgc aacgagaacc ccaacggccc cacggaaggc  1020
tctgaccgct cggcctctc cctcaaccac actattctgg ctggagttca cagcaatgac  1080
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<210> 5

<211> 378

<212> PRT

<213> human

<400> 5

Met Ala Thr Ala Leu Pro Pro Arg Leu Gln Pro Val Arg Gly Asn Glu

5

10

15

Thr Leu Arg Glu His Tyr Gln Tyr Val Gly Lys Leu Ala Gly Arg Leu

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Lys Glu Ala Ser Glu Gly Ser Thr Leu Thr Thr Val Leu Phe Leu Val		
35	40	45
Ile Cys Ser Phe Ile Val Leu Glu Asn Leu Met Val Leu Ile Ala Ile		
50	55	60
Trp Lys Asn Asn Lys Phe His Asn Arg Met Tyr Phe Phe Ile Gly Asn		
65	70	75
80		
Leu Ala Leu Cys Asp Leu Leu Ala Gly Ile Ala Tyr Lys Val Asn Ile		
85	90	95
Leu Met Ser Gly Lys Lys Thr Phe Ser Leu Ser Pro Thr Val Trp Phe		
100	105	110
Leu Arg Glu Gly Ser Met Phe Val Ala Leu Gly Ala Ser Thr Cys Ser		
115	120	125
Leu Leu Ala Ile Ala Ile Glu Arg His Leu Thr Met Ile Lys Met Arg		
130	135	140
Pro Tyr Asp Ala Asn Lys Arg His Arg Val Phe Leu Leu Ile Gly Met		
145	150	155
160		
Cys Trp Leu Ile Ala Phe Thr Leu Gly Ala Leu Pro Ile Leu Gly Trp		
165	170	175
Asn Cys Leu His Asn Leu Pro Asp Cys Ser Thr Ile Leu Pro Leu Tyr		
180	185	190
Ser Lys Lys Tyr Ile Ala Phe Cys Ile Ser Ile Phe Thr Ala Ile Leu		
195	200	205
Val Thr Ile Val Ile Leu Tyr Ala Arg Ile Tyr Phe Leu Val Lys Ser		
210	215	220
Ser Ser Arg Lys Val Ala Asn His Asn Asn Ser Glu Arg Ser Met Ala		
225	230	235
240		
Leu Leu Arg Thr Val Val Ile Val Val Ser Val Phe Ile Ala Cys Trp		
245	250	255
Ser Pro Leu Phe Ile Leu Phe Leu Ile Asp Val Ala Cys Arg Val Gln		
260	265	270
Ala Cys Pro Ile Leu Phe Lys Ala Gln Trp Phe Ile Val Leu Ala Val		
275	280	285
Leu Asn Ser Ala Met Asn Pro Val Ile Tyr Thr Leu Ala Ser Lys Glu		
290	295	300
Met Arg Arg Ala Phe Phe Arg Leu Val Cys Asn Cys Leu Val Arg Gly		
305	310	315
320		

Arg Gly Ala Arg Ala Ser Pro Ile Gln Pro Ala Leu Asp Pro Ser Arg
 325 330 335
 Ser Lys Ser Ser Ser Ser Asn Asn Ser Ser His Ser Pro Lys Val Lys
 340 345 350
 Glu Asp Leu Pro His Thr Asp Pro Ser Ser Cys Ile Met Asp Lys Asn
 355 360 365
 Ala Ala Leu Gln Asn Gly Ile Phe Cys Asn
 370 375

<210> 6

<211> 1134

<212> DNA

<213> human

<400> 6

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ctcaccaccg tgcctcttctt ggtcatctgc agcttcatcg tcttgagaa cctgatggtt 180
ttgattgcc a tctgaaaaa caataaat t cacaaccgca tgtacttttt cattggcaac 240
ctggctctct ggcacctgct ggccggcatc gcttacaagg tcaacattct gatgtctggc 300
aagaagacgt tcagcctgtc tcccacggtc tggttctca gggaggggcag tatgttcgtg 360
gcccttgggg cgtccacctg cagcttactg gccatcgcca tcgagcggca cttgacaatg 420
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aatctccctg actgctctac catctgccc ctctactcca agaagtacat tgccttctgc 600
atcagcatct tcaaggccat cctggtgacc atcgtgatcc tctacgcag catctacttc 660
ctggtgaagt ccagcagccg taaggtggcc aaccacaaca actcggagcg gtccatggca 720
ctgctgcgga ccgtggtgat tgtggtgagc gtgttcatcg cctgctggtc cccactcttc 780
atcctcttcc tcattgatgt ggctgcagg gtgcaggcgt gcccacccct cttcaaggct 840
cagtgttca tcgtgttggc tgtgtcaac tccgcatga acccggtcat ctacacgctg 900
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cggggggccc ggcctcacc catccagcct gcgtcgcacc caagcagaag taaatcaagc 1020
agcagcaaca atagcagcca ctctccgaag gtcaaggaag acctgcccc cagagacccc 1080
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<210> 7

<211> 222

<212> PRT

<213> Rat

<400> 7

Arg Met Tyr Phe Phe Ile Gly Asn Leu Ala Leu Cys Asp Leu Leu Ala
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 Gly Ile Ala Tyr Lys Val Asn Ile Leu Met Ser Gly Arg Lys Thr Phe
 20 25 30
 Ser Leu Ser Pro Thr Val Trp Phe Leu Arg Glu Gly Ser Met Phe Val
 35 40 45
 Ala Leu Gly Ala Ser Thr Cys Ser Leu Leu Ala Ile Ala Ile Glu Arg
 50 55 60
 His Leu Thr Met Ile Lys Met Arg Pro Tyr Asp Ala Asn Lys Lys His
 65 70 75 80
 Arg Val Phe Leu Leu Ile Gly Met Cys Trp Leu Ile Ala Phe Ser Leu
 85 90 95
 Gly Ala Leu Pro Ile Leu Gly Trp Asn Cys Leu Glu Asn Phe Pro Asp
 100 105 110
 Cys Ser Thr Ile Leu Pro Leu Tyr Ser Lys Lys Tyr Ile Ala Phe Leu
 115 120 125
 Ile Ser Ile Phe Thr Ala Ile Leu Val Thr Ile Val Ile Leu Tyr Ala
 130 135 140
 Arg Ile Tyr Phe Leu Val Lys Ser Ser Ser Arg Arg Val Ala Asn His
 145 150 155 160
 Asn Ser Glu Arg Ser Met Ala Leu Leu Arg Thr Val Val Ile Val Val
 165 170 175
 Ser Val Phe Ile Ala Cys Trp Ser Pro Leu Phe Ile Leu Phe Leu Ile
 180 185 190
 Asp Val Ala Cys Arg Ala Lys Glu Cys Ser Ile Leu Phe Lys Ser Gln
 195 200 205
 Trp Phe Ile Met Leu Ala Val Leu Asn Ser Ala Met Asn Pro
 210 215 220

<210> 8

<211> 666

<212> DNA

<213> Rat

<400> 8

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ctcagggagg gcagtatgtt cgtagccctg ggcgcacca catgcagctt attggccatt  180
gccattgagc ggcacctgac catgatcaag atgaggccgt acgacgcaa caagaagcac  240
cgcggtttcc ttctgattgg gatgtgctgg ctaattgect tctcgctggg tgccctgccc  300
atcctgggct ggaactgcct ggagaacttt cccgactgct ctaccatctt gcccctctac  360
tccaagaaat acattgcctt tctcatcagc atcttcacag ccattctggt gaccatcgtc  420
atcttgtaag cgcgcattca cttcctggtc aagtccagca gccgcagggt ggccaaccac  480
aactccgaga gatccatggc ctttctcggg accgtagtga tcgtggtgag cgtgttcac  540
gcctgttggt cccccctttt catcctcttc ctcacgatg tggcctgcag ggccaaggag  600
tgctccatcc tcttcaagag tcagtgggtc atcatgctgg ctgtcctcaa ctccgccatg  660
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<210> 9

<211> 353

<212> PRT

<213> human

<400> 9

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Met Gly Ser Leu Tyr Ser Glu Tyr Leu Asn Pro Asn Lys Val Gln Glu
      5              10              15
His Tyr Asn Tyr Thr Lys Glu Thr Leu Glu Thr Gln Glu Thr Thr Ser
      20              25              30
Arg Gln Val Ala Ser Ala Phe Ile Val Ile Leu Cys Cys Ala Ile Val
      35              40              45
Val Glu Asn Leu Leu Val Leu Ile Ala Val Ala Arg Asn Ser Lys Phe
      50              55              60
His Ser Ala Met Tyr Leu Phe Leu Gly Asn Leu Ala Ala Ser Asp Leu
      65              70              75              80
Leu Ala Gly Val Ala Phe Val Ala Asn Thr Leu Leu Ser Gly Ser Val
      85              90              95
Thr Leu Arg Leu Thr Pro Val Gln Trp Phe Ala Arg Glu Gly Ser Ala
      100             105             110
Ser Ile Thr Leu Ser Ala Ser Val Phe Ser Leu Leu Ala Ile Ala Ile
      115             120             125

```

Glu Arg His Val Ala Ile Ala Lys Val Lys Leu Tyr Gly Ser Asp Lys
 130 135 140
 Ser Cys Arg Met Leu Leu Leu Ile Gly Ala Ser Trp Leu Ile Ser Leu
 145 150 155 160
 Val Leu Gly Gly Leu Pro Ile Leu Gly Trp Asn Cys Leu Gly His Leu
 165 170 175
 Glu Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys His Tyr Val Leu
 180 185 190
 Cys Val Val Thr Ile Phe Ser Ile Ile Leu Leu Ala Ile Val Ala Leu
 195 200 205
 Tyr Val Arg Ile Tyr Cys Val Val Arg Ser Ser His Ala Asp Met Ala
 210 215 220
 Ala Pro Gln Thr Leu Ala Leu Leu Lys Thr Val Thr Ile Val Leu Gly
 225 230 235 240
 Val Phe Ile Val Cys Trp Leu Pro Ala Phe Ser Ile Leu Leu Leu Asp
 245 250 255
 Tyr Ala Cys Pro Val His Ser Cys Pro Ile Leu Tyr Lys Ala His Tyr
 260 265 270
 Phe Phe Ala Val Ser Thr Leu Asn Ser Leu Leu Asn Pro Val Ile Tyr
 275 280 285
 Thr Trp Arg Ser Arg Asp Leu Arg Arg Glu Val Leu Arg Pro Leu Gln
 290 295 300
 Cys Trp Arg Pro Gly Val Gly Val Gln Gly Arg Arg Arg Val Gly Thr
 305 310 315 320
 Pro Gly His His Leu Leu Pro Leu Arg Ser Ser Ser Ser Leu Glu Arg
 325 330 335
 Gly Met His Met Pro Thr Ser Pro Thr Phe Leu Glu Gly Asn Thr Val
 340 345 350
 Val

<210> 10

<211> 1059

<212> DNA

<213> human

<400> 10

atgggcagct tgtactcgga gtacctgaac cccaacaagg tccaggaaca ctataattat 60

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gtcatcctct gttgcgcat tgtggtggaa aaccttctgg tgcctattgc ggtggccga 180
aacagcaagt tccactcggc aatgtacctg tttctgggca acctggccgc ctccgatcta 240
ctggcaggcg tggccttcgt agccaatacc ttgctctctg gctctgtcac gctgaggetg 300
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gtccactcct gcccgatcct ctacaaagcc cactactttt tcgccgtctc caccctgaat 840
tcctgtctca accccgtcat ctacacgtgg cgcagccggg acctgcggcg ggaggtgctt 900
cggccgtgc agtgtgtggc gccgggggtg ggggtgcaag gacggaggcg ggtcgggacc 960
ccgggccacc acctcctgcc actccgcagc tccagctccc tggagagggg catgcacatg 1020
cccacgtcac ccacgtttct ggagggaac acggtggtc 1059

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<210> 11

<211> 352

<212> PRT

<213> Rat

<400> 11

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Met Gly Gly Leu Tyr Ser Glu Tyr Leu Asn Pro Glu Lys Val Gln Glu
      5              10              15
His Tyr Asn Tyr Thr Lys Glu Thr Leu Asp Met Gln Glu Thr Pro Ser
      20              25              30
Arg Lys Val Ala Ser Ala Phe Ile Ile Ile Leu Cys Cys Ala Ile Val
      35              40              45
Val Glu Asn Leu Leu Val Leu Ile Ala Val Ala Arg Asn Ser Lys Phe
      50              55              60
His Ser Ala Met Tyr Leu Phe Leu Gly Asn Leu Ala Ala Ser Asp Leu
      65              70              75              80
Leu Ala Gly Val Ala Phe Val Ala Asn Thr Leu Leu Ser Gly Pro Val
      85              90              95
Thr Leu Ser Leu Thr Pro Leu Gln Trp Phe Ala Arg Glu Gly Ser Ala

```

100	105	110
Phe Ile Thr Leu Ser Ala Ser Val	Phe Ser Leu Leu Ala Ile Ala Ile	
115	120	125
Glu Arg Gln Val Ala Ile Ala Lys Val	Lys Leu Tyr Gly Ser Asp Lys	
130	135	140
Ser Cys Arg Met Leu Met Leu Ile Gly	Ala Ser Trp Leu Ile Ser Leu	
145	150	155
Ile Leu Gly Gly Leu Pro Ile Leu Gly	Trp Asn Cys Leu Asp His Leu	
165	170	175
Glu Ala Cys Ser Thr Val Leu Pro Leu	Tyr Ala Lys His Tyr Val Leu	
180	185	190
Cys Val Val Thr Ile Phe Ser Val Ile	Leu Leu Ala Ile Val Ala Leu	
195	200	205
Tyr Val Arg Ile Tyr Phe Val Val Arg	Ser Ser His Ala Asp Val Ala	
210	215	220
Gly Pro Gln Thr Leu Ala Leu Leu Lys	Thr Val Thr Ile Val Leu Gly	
225	230	235
Val Phe Ile Ile Cys Trp Leu Pro Ala	Phe Ser Ile Leu Leu Leu Asp	
245	250	255
Ser Thr Cys Pro Val Arg Ala Cys Pro	Val Leu Tyr Lys Ala His Tyr	
260	265	270
Phe Phe Ala Phe Ala Thr Leu Asn Ser	Leu Leu Asn Pro Val Ile Tyr	
275	280	285
Thr Trp Arg Ser Arg Asp Leu Arg Arg	Glu Val Leu Arg Pro Leu Leu	
290	295	300
Cys Trp Arg Gln Gly Lys Gly Ala Thr	Gly Arg Arg Gly Gly Asn Pro	
305	310	315
Gly His Arg Leu Leu Pro Leu Arg Ser	Ser Ser Ser Leu Glu Arg Gly	
325	330	335
Leu His Met Pro Thr Ser Pro Thr Phe	Leu Glu Gly Asn Thr Val Val	
340	345	350

<210> 12

<211> 1056

<212> DNA

<213> Rat

<400> 12

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atcatTTTTat.gctgtgccat cgtgggtggag aaccttcttg tgctaatacg agtggccagg   180
aacagcaagt tccactcagc catgtacctg ttcctcggca acctggcagc ctccgacctg   240
ctggcaggcg tggccttcgt ggccaacacc ttgctctccg gacctgtcac cctgtcctta   300
actcccttgc agtggtttgc ccgagagggt tcagccttca tcacgtctc tgccctcggtc   360
ttcagcctcc tggccattgc catcgagaga caagtggcca tcgccaaggt caagctctac   420
ggcagtgaca aaagctgtcg aatgttgatg ctcatgggg cctcttggt gatatcgctg   480
attctgggtg gcttgcccat cctgggctgg aattgtcttg accatctgga ggcttgcctc   540
actgtgtgc ccctctatgc taagcactat gtgctctgcg tggtcaccat cttctctgtc   600
atcttactgg ctatcgtggc cttgtacgtc cgaatctact tcgtagtccg ctcaagccat   660
gcggacgttg ctggtcctca gacgttgcc ctgctcaaga cagtcaccat cgtactgggt   720
gttttcatca tctgtgggt gccggctttt agcatccttc tcttagactc tacctgtccc   780
gtccgggect gtctgtcct ctacaaagcc cattatttct ttgccttcgc caccctcaac   840
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